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1209

#2

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/922,067

DATE: 11/19/2001

TIME: 09:46:22

Input Set : N:\Crf3\RULE60\09922067.raw

Output Set: N:\CRF3\11192001\I922067.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: MacPhee, Colin Houston

6 Tew, David Graham

7 Southan, Christopher Donald

8 Hickey, Dierdre Mary Bernadette

9 Gloger, Israel Simon

10 Lawrence, Geoffrey Mark Prouse

11 Rice, Simon Quantyn John

13 (ii) TITLE OF INVENTION: Lipoprotein Associated Phospholipase A2, Inhibitors  
14 Thereof And Use Of The Same In Diagnosis And Therapy

16 (iii) NUMBER OF SEQUENCES: 11

18 (iv) CORRESPONDENCE ADDRESS:

19 (A) ADDRESSEE: SmithKline Beecham Corporation

20 (B) STREET: 709 Swedeland Road

21 (C) CITY: King of Prussia

22 (D) STATE: PA

23 (E) COUNTRY: USA

24 (F) ZIP: 19406

26 (v) COMPUTER READABLE FORM:

27 (A) MEDIUM TYPE: Diskette

28 (B) COMPUTER: IBM PC compatible

29 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

30 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

32 (vi) CURRENT APPLICATION DATA:

C--&gt; 33 (A) APPLICATION NUMBER: US/09/922,067

C--&gt; 34 (B) FILING DATE: 03-Aug-2001

35 (C) CLASSIFICATION:

37 (vii) PRIOR APPLICATION DATA:

38 (A) APPLICATION NUMBER: 09/193,130

39 (B) FILING DATE: 1998-11-17

41 (A) APPLICATION NUMBER: PCT/GB94/01374

42 (B) FILING DATE: 24 June 1994

44 (viii) ATTORNEY/AGENT INFORMATION:

45 (A) NAME: Dustman, Wayne J.

46 (B) REGISTRATION NUMBER: 33,870

47 (C) REFERENCE/DOCKET NUMBER: P30693

49 (ix) TELECOMMUNICATION INFORMATION:

50 (A) TELEPHONE: 610-270-5023

51 (B) TELEFAX: 610-270-5090

52 (C) TELEX:

54 (2) INFORMATION FOR SEQ ID NO: 1:

56 (i) SEQUENCE CHARACTERISTICS:

57 (A) LENGTH: 37 amino acids

58 (B) TYPE: amino acid

59 (C) STRANDEDNESS:

60 (D) TOPOLOGY: linear

ENTERED

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62      (ii) MOLECULE TYPE: peptide
64      (iii) HYPOTHETICAL: NO
C--> 68      (v) FRAGMENT TYPE: internal
70      (vi) ORIGINAL SOURCE:
C--> 72      (ix) FEATURE:
74      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
76      Met Leu Lys Leu Lys Gly Asp Ile Asp Ser Asn Ala Ala Ile Asp Leu
77      1           5           10           15
79      Ser Asn Lys Ala Ser Leu Ala Phe Leu Gln Lys His Leu Gly Leu His
80      20           25           30
82      Lys Asp Phe Asp Gln
83      35
85 (2) INFORMATION FOR SEQ ID NO: 2:
87      (i) SEQUENCE CHARACTERISTICS:
88          (A) LENGTH: 30 amino acids
89          (B) TYPE: amino acid
90          (D) TOPOLOGY: linear
92      (ii) MOLECULE TYPE: peptide
94      (iii) HYPOTHETICAL: NO
96      (v) FRAGMENT TYPE: internal
100     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
102     Trp Met Phe Pro Leu Gly Asp Glu Val Tyr Ser Arg Ile Pro Gln Pro
103     1           5           10           15
105     Leu Phe Phe Ile Asn Ser Glu Tyr Phe Gln Tyr Pro Ala Asn
106     20           25           30
108 (2) INFORMATION FOR SEQ ID NO: 3:
110     (i) SEQUENCE CHARACTERISTICS:
111         (A) LENGTH: 27 amino acids
112         (B) TYPE: amino acid
113         (D) TOPOLOGY: linear
115     (ii) MOLECULE TYPE: peptide
117     (iii) HYPOTHETICAL: NO
119     (v) FRAGMENT TYPE: internal
123     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
125     Gln Tyr Ile Asn Pro Ala Val Met Ile Thr Ile Arg Gly Ser Val His
126     1           5           10           15
128     Gln Asn Phe Ala Asp Phe Thr Phe Ala Thr Gly
129     20           25
131 (2) INFORMATION FOR SEQ ID NO: 4:
133     (i) SEQUENCE CHARACTERISTICS:
134         (A) LENGTH: 19 amino acids
135         (B) TYPE: amino acid
136         (D) TOPOLOGY: linear
138     (ii) MOLECULE TYPE: peptide
140     (iii) HYPOTHETICAL: NO
142     (v) FRAGMENT TYPE: internal
146     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
148     Trp Leu Met Gly Asn Ile Leu Arg Leu Leu Phe Gly Ser Met Thr Thr
149     1           5           10           15

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151      Pro Ala Asn
154 (2) INFORMATION FOR SEQ ID NO: 5:
156      (i) SEQUENCE CHARACTERISTICS:
157          (A) LENGTH: 420 base pairs
158          (B) TYPE: nucleic acid
159          (C) STRANDEDNESS: double
160          (D) TOPOLOGY: linear
162      (ii) MOLECULE TYPE: cDNA
164      (iii) HYPOTHETICAL: NO
C--> 166      (iv) ANTI-SENSE: NO
170      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
172 AAAAAACCTA TTTTAATCCT AATTGTATTT CTCTATTCCT GAAGAGTTCT GTAACATGAT      60
174 GTGTTGATTG GTTGTGTAA TGTGGTCCC TGGAATAAGA TTCTCATCAT CTCCTTCAAT      120
176 CAAGCAGTCC CACTGATCAA AATCTTTATG AAGTCCTAAA TGCTTTTGTA AGAATGCTAA      180
178 TGAAGCTTTG TTGCTAAGAT CAATAGCTGC ATTTGAATCT ATGTCTCCCT TTAATTTGAG      240
180 CATGTGTCCA ATTATTTTGC CAGTNGCAA AGTGAAGTCA GCAAATTCT GGTGGACTGA      300
182 ACCCCTGATT GTAATCATCT TTCTTTCTTT ATCAGGTGAG TAGCATTTT TCATTTTAT      360
184 GATATTAGCA GGATATTGGA AATATTCAGN GTTGNTAAAA AGNGGNGGCT GAGGGATTCT      420
187 (2) INFORMATION FOR SEQ ID NO: 6:
189      (i) SEQUENCE CHARACTERISTICS:
190          (A) LENGTH: 379 base pairs
191          (B) TYPE: nucleic acid
192          (C) STRANDEDNESS: double
193          (D) TOPOLOGY: linear
195      (ii) MOLECULE TYPE: cDNA
197      (iii) HYPOTHETICAL: NO
C--> 199      (iv) ANTI-SENSE: NO
203      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
205 TGCTAATATC ATAAAAATGA AAAAATGCTA CTCACCTGAT AAAGAAAGAA AGATGATTAC      60
207 AATCAGGGGT TCAGTCCACC AGANTTTTGC TGACTTCACT TTTGCAACTG GCAAAATAAT      120
209 TGGACACATG CTCAAATTAA AGGGAGACAT AGATTCAAAT GTAGCTATTG ATCTTAGCAA      180
211 CAAAGCTTCA TTAGCATTTCT TACAAAAGCA TTTAGGACTT CATAAAGATT TTGTTTCAGTG      240
213 GGACTGCTTG ATTGAAGGAG ATGATGAGAA TCTTATTCCA GGGACCAACA TTAACACAAC      300
215 CAATTCAACA CATCATGTTT ACAGAACTTC TTCCAGGGAA TAGGAGGAAA TACAATTGGG      360
217 GTTTAAAAATA GTTTTTTTTT
                                           379
219 (2) INFORMATION FOR SEQ ID NO: 7:
221      (i) SEQUENCE CHARACTERISTICS:
222          (A) LENGTH: 279 base pairs
223          (B) TYPE: nucleic acid
224          (C) STRANDEDNESS: double
225          (D) TOPOLOGY: linear
227      (ii) MOLECULE TYPE: cDNA
229      (iii) HYPOTHETICAL: NO
C--> 231      (iv) ANTI-SENSE: NO
235      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
237 GAAGAATGCA TTAGATTTAA AGTTTGATAT GGAACAACCTG AAGGACTCTA TTGATAGGGA      60
239 AAAAATAGCA GTAATTGGAC ATTCTTTTGG TGGAGCAACG GTTATTCAGA CTCTTAGTGA      120
241 AGATCAGAGA TTCAGATGTG GTATTGCCCT GGATGCATGG ATGTTTCCAC TGGGTGATGA      180
243 AGTATATTCC AGAATTCCTC AGCCCCTCTT TTTTATCAAC TCTGAATATT TCCAATATCC      240

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245 TGCTAATATC ATAAANTGG AAAATGCTA CTCACCTGG
247 (2) INFORMATION FOR SEQ ID NO: 8:
249     (i) SEQUENCE CHARACTERISTICS:
250         (A) LENGTH: 572 base pairs
251         (B) TYPE: nucleic acid
252         (C) STRANDEDNESS: double
253         (D) TOPOLOGY: linear
255     (ii) MOLECULE TYPE: cDNA
257     (iii) HYPOTHETICAL: NO
C--> 259     (iv) ANTI-SENSE: NO
263     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
265 AAAATAGCAG TAATTGGACA TTCTTTAGGT GGAGCAACGG TTATTCAGAC TCTTAGTGAA      60
267 GATCAGAGAT TCAGATGTGG TATTGCCCTG GATGCATGGA TGTTTCCACT GGGTGATGAA      120
269 GTATATTCCA GAATTCCTCA GCCCCTCTTT TTTATCAACT CTGAATATTT CCAATATCCT      180
271 GCTAATATCA TAAAAATGAA AAAATGCTAC TCACCTGATA AAGAAAGAAA GATGATTACA      240
273 ATCAGGGGTT CAGTCCACCA GAATTTTGCT GACTTCACTT TTGCAACTGG CAAAATAATT      300
275 GGACACATGC TCAAATTAAA GGGAGACATA GATTCAAATG TAGCTATTGA TCTTAGCAAC      360
277 AAAGCTTCAT CAGCATTCTT ACAAAGCAT TTAGGACTTC ATAAAGATT TGATCAGTGG      420
279 GACTGCTTGA TTGAAGGAGA TGATGAGAAT CTTATTCCAG GGACCAACAT TAACACAACC      480
281 AATCAACACA TCATGTTACA GAACTCTTCA GGAATAGAGA AATACAATTA GGATTAAAT      540
283 AGGTTTTTTT AAAAAAAAAA AAAAAAACT CG      572
285 (2) INFORMATION FOR SEQ ID NO: 9:
287     (i) SEQUENCE CHARACTERISTICS:
288         (A) LENGTH: 1361 base pairs
289         (B) TYPE: nucleic acid
290         (C) STRANDEDNESS: double
291         (D) TOPOLOGY: linear
293     (ii) MOLECULE TYPE: cDNA
295     (iii) HYPOTHETICAL: NO
C--> 297     (iv) ANTI-SENSE: NO
300     (ix) FEATURE:
301         (A) NAME/KEY: CDS
302         (B) LOCATION: 38..1360
305     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
307 TGAGAGACTA AGCTGAAACT GCTGCTCAGC TCCCAAG ATG GTG CCA CCC AAA TTG      55
308                                     Met Val Pro Pro Lys Leu
309                                     1           5
311 CAT GTG CTT TTC TGC CTC TGC GGC TGC CTG GCT GTG GTT TAT CCT TTT      103
312 His Val Leu Phe Cys Leu Cys Gly Cys Leu Ala Val Val Tyr Pro Phe
313         10           15           20
315 GAC TGG CAA TAC ATA AAT CCT GTT GCC CAT ATG AAA TCA TCA GCA TGG      151
316 Asp Trp Gln Tyr Ile Asn Pro Val Ala His Met Lys Ser Ser Ala Trp
317         25           30           35
319 GTC AAC AAA ATA CAA GTA CTG ATG GCT GCT GCA AGC TTT GGC CAA ACT      199
320 Val Asn Lys Ile Gln Val Leu Met Ala Ala Ala Ser Phe Gly Gln Thr
321         40           45           50
323 AAA ATC CCC CGG GGA AAT GGG CCT TAT TCC GTT GGT TGT ACA GAC TTA      247
324 Lys Ile Pro Arg Gly Asn Gly Pro Tyr Ser Val Gly Cys Thr Asp Leu
325 55           60           65           70

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| 327 | ATG | TTT | GAT | CAC | ACT | AAT | AAG | GGC | ACC | TTC | TTG | CGT | TTA | TAT | TAT | CCA | 295  |
| 328 | Met | Phe | Asp | His | Thr | Asn | Lys | Gly | Thr | Phe | Leu | Arg | Leu | Tyr | Tyr | Pro |      |
| 329 |     |     |     |     | 75  |     |     |     |     | 80  |     |     |     |     |     | 85  |      |
| 331 | TCC | CAA | GAT | AAT | GAT | CGC | CTT | GAC | ACC | CTT | TGG | ATC | CCA | AAT | AAA | GAA | 343  |
| 332 | Ser | Gln | Asp | Asn | Asp | Arg | Leu | Asp | Thr | Leu | Trp | Ile | Pro | Asn | Lys | Glu |      |
| 333 |     |     |     | 90  |     |     |     |     | 95  |     |     |     |     | 100 |     |     |      |
| 335 | TAT | TTT | TGG | GGT | CTT | AGC | AAA | TTT | CTT | GGA | ACA | CAC | TGG | CTT | ATG | GGC | 391  |
| 336 | Tyr | Phe | Trp | Gly | Leu | Ser | Lys | Phe | Leu | Gly | Thr | His | Trp | Leu | Met | Gly |      |
| 337 |     |     | 105 |     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |      |
| 339 | AAC | ATT | TTG | AGG | TTA | CTC | TTT | GGT | TCA | ATG | ACA | ACT | CCT | GCA | AAC | TGG | 439  |
| 340 | Asn | Ile | Leu | Arg | Leu | Leu | Phe | Gly | Ser | Met | Thr | Thr | Pro | Ala | Asn | Trp |      |
| 341 |     | 120 |     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     |      |
| 343 | AAT | TCC | CCT | CTG | AGG | CCT | GGT | GAA | AAA | TAT | CCA | CTT | GTT | GTT | TTT | TCT | 487  |
| 344 | Asn | Ser | Pro | Leu | Arg | Pro | Gly | Glu | Lys | Tyr | Pro | Leu | Val | Val | Phe | Ser |      |
| 345 | 135 |     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |      |
| 347 | CAT | GGT | CTT | GGG | GCA | TTC | AGG | ACA | CTT | TAT | TCT | GCT | ATT | GGC | ATT | GAC | 535  |
| 348 | His | Gly | Leu | Gly | Ala | Phe | Arg | Thr | Leu | Tyr | Ser | Ala | Ile | Gly | Ile | Asp |      |
| 349 |     |     |     | 155 |     |     |     |     | 160 |     |     |     |     | 165 |     |     |      |
| 351 | CTG | GCA | TCT | CAT | GGG | TTT | ATA | GTT | GCT | GCT | GTA | GAA | CAC | AGA | GAT | AGA | 583  |
| 352 | Leu | Ala | Ser | His | Gly | Phe | Ile | Val | Ala | Ala | Val | Glu | His | Arg | Asp | Arg |      |
| 353 |     |     |     | 170 |     |     |     |     | 175 |     |     |     |     | 180 |     |     |      |
| 355 | TCT | GCA | TCT | GCA | ACT | TAC | TAT | TTC | AAG | GAC | CAA | TCT | GCT | GCA | GAA | ATA | 631  |
| 356 | Ser | Ala | Ser | Ala | Thr | Tyr | Tyr | Phe | Lys | Asp | Gln | Ser | Ala | Ala | Glu | Ile |      |
| 357 |     |     | 185 |     |     |     |     | 190 |     |     |     |     | 195 |     |     |     |      |
| 359 | GGG | GAC | AAG | TCT | TGG | CTC | TAC | CTT | AGA | ACC | CTG | AAA | CAA | GAG | GAG | GAG | 679  |
| 360 | Gly | Asp | Lys | Ser | Trp | Leu | Tyr | Leu | Arg | Thr | Leu | Lys | Gln | Glu | Glu | Glu |      |
| 361 |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |     |     |     |     |      |
| 363 | ACA | CAT | ATA | CGA | AAT | GAG | CAG | GTA | CGG | CAA | AGA | GCA | AAA | GAA | TGT | TCC | 727  |
| 364 | Thr | His | Ile | Arg | Asn | Glu | Gln | Val | Arg | Gln | Arg | Ala | Lys | Glu | Cys | Ser |      |
| 365 | 215 |     |     |     |     | 220 |     |     |     |     | 225 |     |     |     |     | 230 |      |
| 367 | CAA | GCT | CTC | AGT | CTG | ATT | CTT | GAC | ATT | GAT | CAT | GGA | AAG | CCA | GTG | AAG | 775  |
| 368 | Gln | Ala | Leu | Ser | Leu | Ile | Leu | Asp | Ile | Asp | His | Gly | Lys | Pro | Val | Lys |      |
| 369 |     |     |     | 235 |     |     |     |     | 240 |     |     |     |     | 245 |     |     |      |
| 371 | AAT | GCA | TTA | GAT | TTA | AAG | TTT | GAT | ATG | GAA | CAA | CTG | AAG | GAC | TCT | ATT | 823  |
| 372 | Asn | Ala | Leu | Asp | Leu | Lys | Phe | Asp | Met | Glu | Gln | Leu | Lys | Asp | Ser | Ile |      |
| 373 |     |     |     | 250 |     |     |     |     | 255 |     |     |     |     | 260 |     |     |      |
| 375 | GAT | AGG | GAA | AAA | ATA | GCA | GTA | ATT | GGA | CAT | TCT | TTT | GGT | GGA | GCA | ACG | 871  |
| 376 | Asp | Arg | Glu | Lys | Ile | Ala | Val | Ile | Gly | His | Ser | Phe | Gly | Gly | Ala | Thr |      |
| 377 |     |     | 265 |     |     |     |     | 270 |     |     |     |     | 275 |     |     |     |      |
| 379 | GTT | ATT | CAG | ACT | CTT | AGT | GAA | GAT | CAG | AGA | TTC | AGA | TGT | GGT | ATT | GCC | 919  |
| 380 | Val | Ile | Gln | Thr | Leu | Ser | Glu | Asp | Gln | Arg | Phe | Arg | Cys | Gly | Ile | Ala |      |
| 381 |     | 280 |     |     |     |     | 285 |     |     |     |     | 290 |     |     |     |     |      |
| 383 | CTG | GAT | GCA | TGG | ATG | TTT | CCA | CTG | GGT | GAT | GAA | GTA | TAT | TCC | AGA | ATT | 967  |
| 384 | Leu | Asp | Ala | Trp | Met | Phe | Pro | Leu | Gly | Asp | Glu | Val | Tyr | Ser | Arg | Ile |      |
| 385 | 295 |     |     |     |     | 300 |     |     |     |     | 305 |     |     |     |     | 310 |      |
| 387 | CCT | CAG | CCC | CTC | TTT | TTT | ATC | AAC | TCT | GAA | TAT | TTC | CAA | TAT | CCT | GCT | 1015 |
| 388 | Pro | Gln | Pro | Leu | Phe | Phe | Ile | Asn | Ser | Glu | Tyr | Phe | Gln | Tyr | Pro | Ala |      |
| 389 |     |     |     | 315 |     |     |     |     | 320 |     |     |     |     | 325 |     |     |      |
| 391 | AAT | ATC | ATA | AAA | ATG | AAA | AAA | TGC | TAC | TCA | CCT | GAT | AAA | GAA | AGA | AAG | 1063 |

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/922,067

DATE: 11/19/2001

TIME: 09:46:23

Input Set : N:\Crf3\RULE60\09922067.raw

Output Set: N:\CRF3\11192001\I922067.raw

L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:66 M:220 C: Keyword misspelled or invalid format, [(v) FRAGMENT TYPE:]  
L:72 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]  
L:74 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=1  
L:166 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:199 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:231 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:259 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:297 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]